

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 16:16:11 ; Search time 15.6881 seconds
(without alignments)
2330.584 Million cell updates/sec

Title: US-10-003-356-5
Perfect score: 1986
Sequence: 1 LEHSSVCTDVCPPGTRGGFQ.....TVSTVLDDDRVLIYMCPLRLQ 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries

Database : PIR_79;*: 1: pir1;*: 2: pir2;*: 3: pir3;*: 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	714.5		36.0	1079	2	I59362	calcium/polyvalent calcium receptor (calcium receptor (calcium receptor (Ca(2+)-sensing receptor TIR taste receptor TIR metabotropic gluta metabotropic gluta metabotropic gluta metabotropic gluta metabotropic gluta G protein-coupled metabotropic gluta metabotropic gluta glutamate receptor hypothetical prote metabotropic gluta hypothetical prote metabotropic gluta metabotropic gluta metabotropic gluta hypothetical prote hypothetical prote Na+/H+ antiporter bridge of sevenless NADH2 dehydrogenas gene boss protein bridge of sevenless hypothetical prote hypothetical prote
2	711.5		35.8	1078	2	A56715	
3	711.5		35.8	1088	2	B56715	
4	709.5		35.7	1085	2	S40476	
5	431.5		21.7	858	2	JC7683	
6	415.5		20.9	879	2	JC7160	
7	415.5		20.9	879	2	JH0562	
8	409.5		20.6	872	2	JH0561	
9	397.5		20.0	1180	2	JC2132	
10	397.5		20.0	1199	2	A41939	
11	397.5		20.0	1212	2	JC2131	
12	396.5		20.0	1171	2	A42916	
13	383		19.3	1218	2	S71376	
14	353		17.8	999	2	T27628	
15	324		16.3	915	2	A49874	
16	323		16.3	1267	2	TR1340	
17	309		15.6	871	2	A46742	
18	308		15.5	912	2	JH0563	
19	295		14.9	908	2	I49142	
20	284.5		14.3	551	2	T30806	
21	207.5		10.4	1099	2	T16283	
22	125		6.3	354	2	T33395	
23	119		6.0	377	2	A69277	
24	117		5.9	893	2	A47550	
25	115.5		5.8	486	2	S51503	
26	112		5.6	896	2	S26740	
27	112		5.6	896	2	A36455	
28	110.5		5.6	410	2	E84998	
29	109		5.5	332	2	T21399	

ALIGNMENTS

30	108.5	5.5	403	2	G71236	hypothetical prote
31	108	5.4	464	2	B64173	hypothetical prote
32	105	5.3	887	2	S73768	MG277 homolog F11-secDF protein, pro-
33	104.5	5.3	1400	2	A81672	NADH2 dehydrogenas
34	104	5.2	437	2	A88942	probable membrane protein, R13D11.3 [
35	103.5	5.2	469	2	D84949	hypothetical prote
36	103	5.2	411	2	AF0203	transport ATP-bind
37	103	5.2	552	2	T25496	hypothetical prote
38	103	5.2	592	2	E82939	probable membrane
39	102	5.1	405	2	F89930	hypothetical prote
40	102	5.1	540	2	T43747	NADH2 dehydrogenas
41	100.5	5.1	610	2	S19461	probable membrane
42	100.5	5.1	825	2	T46311	hypothetical prote
43	100	5.0	437	2	H47070	probable O-antigen
44	100	5.0	461	2	H64636	proline/betaine tr
45	99.5	5.0	344	2	T30984	hypothetical prote

RESULT 1

I59362	calcium/polyvalent cation-sensing receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)	
C;Date: 02-Jul-1996 #sequence_change 09-Jul-2004	
C;Accession: I59362; A55594	
R;Ruat, M.; Molliver, M.B.; Snowman, A.M.; Snyder, S.H.	
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995	
A;Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve t.	
A;Reference number: A55594; PMID: 7816802	
A;Accession: A55594	
A;Molecule type: mRNA	
A;Residues: 1-1079 <RES>	
A;Cross-references: UNIPROT:P48442; EMBL:U20289; PIDN:9790578; PIDN: AAC52195.1; PID:9790	
A;Experimental source: striatal	
R;Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, B.M.; Hebert, S.C.	
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995	
A;Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval-	
A;Reference number: A55594	
A;Accession: A55594	
A;Molecule type: mRNA	
A;Residues: 1-133, 'X', 135-1079 <RIC>	
A;Cross-references: GB:U10354	
A;Experimental source: kidney	
C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein	
P;1-20/Domain: signal sequence #status predicted <SIG>	
P;187-212/Region: hydrophobic	
F;613-635/Domain: transmembrane #status predicted <TM1>	
F;650-670/Domain: transmembrane #status predicted <TM2>	
F;683-700/Domain: transmembrane #status predicted <TM3>	
F;725-744/Domain: transmembrane #status predicted <TM4>	
F;770-790/Domain: transmembrane #status predicted <TM5>	
F;806-828/Domain: transmembrane #status predicted <TM6>	
F;841-860/Domain: transmembrane #status predicted <TM7>	
F;90,261,287,386,468,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #status predicted	
F;794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted	
F;899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted	
Query Match Score 36.0*; Pred. No. 38.3*; Length 1079;	
Best Local Similarity 38.3%; Mismatches 71; Indels 27; Gaps 6;	
Matches 146; Conservative 146;	
QY 1 LPHSVCTDVCPGPVGFRQREBPICCFDISPCADGHVSRKPGERECEOCGEDWNSNAQKS 60	
Db 537 VPPSNCSRDQCAGTRKGIIEGBPPTCCFECVPDPGEYSGETDASACDKCPDDFWSNENHR 596	
QY 1 ECVLKEVEYLAYDEALGFTLVILSYFGAFLVAVTAVVYIHRHTPLVNADWQLGFLIQQ 120	
Db 597 SCIAKIEFLAWTEPFGIAITLPLAVLGIFLTAFLVATRNELSYLLFP 656	
QY 121 SLIMLSSMLPIDKPHNWSCMAGQVTLALGFSLCLSLLGKTSSLPLAYRISKSKTQLT 180	

RESULT 2

657 SLLCCPSSSLPPIGEQPDWTCRLRQPAFGISFVLCISCILVKTRNRVLLVF---EAKIP-T 712
 181 SMHPLYRK-----IIVLISVLAEIGCTAYLILEPPMVYKOMESONTKILLGCNEIS 232
 713 SFH---RKWWGLNMQFLVFLCTFMQILICIWLYTAPPSSYRNHELEDEIIFITCHEGGS 769
 QY 233 IEFLYSMFGIDAFIALLCFLTFVARQLPDPNYYEKGKICITFGMLVYFFIIMWSFPVYLSTK 292
 Db 770 LMALGSLIGYTCLAAICFFAFKSRLPENNEAKFITFSMLIFFIWIISFIPAYASTY 829
 QY 293 GKFKMVAEVIFAILASSHGLLGCFAPKCLLILLRPERNTSEIVCGRVSTTDNCIQLTSAF 352
 Db 830 GKFVSAVEVIAILAAASFGLLACIFFNKVYIILFKPSRNTIEEV--RSSTAAGHAFKVAARA 887
 QY 353 V-----SSELNNTTVS 363
 Db 888 TLRRPNTISKRSRSSSLGGSTGS 908

Query Match 35.8%; Score 711.5; DB 2; Length 1078;
 Best Local Similarity 38.0%; Pred. No. 8.3e-50;
 Matches 145; Conservative 71; Mismatches 139; Indels 27; Gaps 6;

1 LPHSVCTDVCPGPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQKS 60
 537 VPFNSNCSDRDLAGTRKGIIIEGPTCCFECVCPDGEYSDETDASACKCPDDFWSNENHT 596

Qy 61 ECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHTPLVNASDWQLGFLIQV 120
 Db 597 SCIAKEIEFLSWTEPFGIAILTFLAVLGIFLTAFVLGPKFRNTPIVKATNRRELSYLLF 656
 Qy 121 SLIIMLSSMLPIDKPHNWSCMAGQVTLALGFSLCLSCLLGKTSSLFLAYRISKSKTQLT 180
 Db 657 SLIICCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLVF---EAKIP-T 712
 Qy 181 SMHPLYRK-----IIVLISVLAEIGCTAYLILEPPMVYKOMESONTKILLGCNEIS 232
 Db 713 SFH---RKWWGLNMQFLVFLCTMFQIVICVWLTYTAPPSSYRNQELEDIIFITCHEGS 769
 Qy 233 IEFLYSMFGIDAFIALLCFLTFVARQLPDPNYYEKGKICITFGMLVYFFIIMWSFPVYLSTK 292
 Db 770 LMALGFLIGYTCLAAICFFAFKSRLPENNEAKPITFSMLIFFIWIISFIPAYASTY 829
 Qy 293 GKFKMVAEVIFAILASSHGLLGCFAPKCLLILLRPERNTSEIVCGRVSTTDNCIQLTSAF 352
 Db 830 GKFKVSAVEVIAILAAASFGLLACIFFNKIVIILFKPSRNTIEEV--RCSTAAHAFKVAARA 887
 A;Accession: A56715
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1078 <GAR>
 A;Cross-references: GB:U20759; NID:9683744; PID:AAA86503.1; PID:9683745
 R;Pearce, S.H.S.; Thakker, R.V.
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 01-Dec-2000
 C;Accession: A56715; S49341; A49419; B49419; C49419
 R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
 J. Biol. Chem. 270, 12919-12925, 1995
 A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
 A;Reference number: A56715; MUID:95279439; PMID:7759551
 A;Accession: A56715
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1078 <GAR>
 A;Cross-references: GB:U20759; NID:9683744; PID:AAA86503.1; PID:9683745
 R;Pearce, S.H.S.; Thakker, R.V.
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
 C;Accession: S49341
 A;Accession: S49341
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>
 A;Cross-references: EMBL:X81086
 R;Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, Cell 75, 1297-1303, 1993
 A;Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuria
 A;Reference number: A49419; MUID:94094324; PMID:7916660
 A;Accession: A49419
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 178-192 <POL>
 A;Experimental source: family N
 A;Note: sequence inconsistent with nucleotide translation
 A;Note: sequence modified after extraction from NCBI backbone
 A;Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and nec
 A;Note: sequence extracted from NCBI backbone (NCBIN:142453)
 A;Accession: B49419
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 289-303 <PO2>
 A;Experimental source: family E
 A;Note: sequence modified after extraction from NCBI backbone
 A;Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and nec
 A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
 A;Accession: C49419
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 788-802 <PO3>
 A;Experimental source: family J
 A;Note: sequence modified after extraction from NCBI backbone
 A;Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and nec
 A;Note: sequence extracted from NCBI backbone (NCBIN:142457)
 C;Keywords: glycoprotein; receptor; transmembrane protein

RESULT 3

B56715 calcium receptor (clone phPCaR-5.2) - human
 C;Species: Homo sapiens (man)
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
 C;Accession: B56715
 R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
 J. Biol. Chem. 270, 12919-12925, 1995
 A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
 A;Reference number: A56715; MUID:95279439; PMID:7759551
 A;Accession: B56715
 A;Status: preliminary
 A;Molecule type: tRNA
 A;Residues: 1-1088 <GAR>
 A;Cross-references: GB:U20760; NID:9683746; PID:AAA86504.1; PID:9683747
 C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 35.8%; Score 711.5; DB 2; Length 1088;
 Best Local Similarity 38.0%; Pred. No. 8.3e-50;
 Matches 145; Conservative 71; Mismatches 139; Indels 27; Gaps 6;

1 LPHSVCTDVCPGPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQKS 60
 547 VPFNSNCSDRDLAGTRKGIIIEGPTCCFECVCPDGEYSDETDASACKCPDDFWSNENHT 606

Qy 61 ECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHTPLVNASDWQLGFLIQV 120
 Db 607 SCIAKEIEFLSWTEPFGIAILTFLAVLGIFLTAFVLGPKFRNTPIVKATNRRELSYLLF 666
 Qy 121 SLIIMLSSMLPIDKPHNWSCMAGQVTLALGFSLCLSCLLGKTSSLFLAYRISKSKTQLT 180
 Db 667 SLIICCFSSSLFFIGEPQDWTCLRQPAFGISFVLCISCLVKTNRVLVF---EAKIP-T 722
 Qy 181 SMHPLYRK-----IIVLISVLAEIGCTAYLILEPPMVYKOMESONTKILLGCNEIS 232
 Db 723 SFH---RKWWGLNMQFLVFLCTMFQIVICVWLTYTAPPSSYRNQELEDIIFITCHEGS 779
 Qy 233 IEFLYSMFGIDAFIALLCFLTFVARQLPDPNYYEKGKICITFGMLVYFFIIMWSFPVYLSTK 292
 C;Keywords: glycoprotein; receptor; transmembrane protein

Db	780 LMALGFLIGYTCLAAICFFFAFKSRKLPEFNNEAKFITSMLIFFIVVISFIPIAYASTY	839	A; Residues: 1-858 <KIT> A; Cross-references: UNIPROT:Q91VA4; DDBJ:AB049994 C; Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the si; C; Genetics: A; Gene: tir3 A; Map position: 4 C; Superfamily: metabotropic glutamate receptor 4 C; Keywords: transmembrane protein
Qy	293 GKFKMVAEPIAILASSHGLLGCIFAPKCLIIILRPERNTSEIVCGRVSTTDNCIQLTSAF	352	
Db	840 GKFVSAEVIAILASFGLLACIFFNKVYIILFKPSRNTIEEV--RCSTAHAHKVVARA	897	
Qy	353 V-----SSELNNTTYST 364		
Db	898 TLRRSNVSRQRSSSLGGSTGST 919		
RESULT 4			
S40476	Ca(2+)-sensing receptor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004		
C;Accession: S40476	R;Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; Nature 366, 575-580, 1993 A;Title: Cloning and characterization of an extracellular Ca (2+)-sensing receptor from b A;Reference number: S40476; MUID:94077182; PMID:8255296		
A;Accession: S40476	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1085 <BRO> A;Cross-references: UNIPROT:P35384; GB:S67307; NID:9453108; PIDN:AAB29171.1; PID:g453109		
Qy	Query Match Score 35.7%; Best Local Similarity 38.0%; Pred. No. 1.2e-49; Matches 145; Conservative 72; Mismatches 138; Indels 27; Gaps 6;		
Db	538 VPPSNCSRQDCLAGTRKGIIIGEPTCCFECVCPDGKYSDETDASACDKCPDFWSNENHT 597		
Qy	1 LPHSVCTTDVCPGTRGFVOREPICCFDSIPCAADGHVSRKPGERECEBQCGEDYWSNAQKS 60		
Db	61 ECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVVYIHRHPTLVNADWQLGFLIQV 120		
Qy	614 SFH---RKWFGLNQFLVPLCTFMQIVICAIWNTAPPSSYRNHELEDEIIFTCHEGS 770		
Db	598 SCIKEIEFLSWTEPFGIALTLPAVLGIFLTAFVLGFIPIKFRNTPIVKATNRELSSYLLLF 657		
Qy	121 SLIIMLSSMLFIDKPHNWSCMAGQVTLALGFLSCLLGKTISSLFLAYRISKSTQLT 180		
Db	658 SLLCCFSSSLFFIGEPQDWTRCLRQPAFGISFVLCSICLVRKTNRVLVF---EAKIP-T 713		
Qy	181 SMHPLYRK-----IVLVLISVLAEGICTAYLILEPPMVYKNMESONTKIIILGCNBIS 232		
Db	714 SFH---RKWFGLNQFLVPLCTFMQIVICAIWNTAPPSSYRNHELEDEIIFTCHEGS 770		
Qy	233 IEFLYSMMPGIDAFALLCFLTTFVARQLPDNYYEKGKCITFGMLVFFIIMSFVPVYLSRK 292		
Db	771 LMALGFLIGYTCLAAICFFFAFKSRKLPEFNNEAKFITSMLIFFIVVISFIPIAYASTY 830		
Qy	293 GKFKMVAEPIAILASSHGLLGCIFAPKCLIIILRPERNTSEIVCGRVSTTDNCIQLTSAF	352	
Db	831 GKFVSAEVIAILASFGLLACIFFNKVYIILFKPSRNTIEEV--RCSTAHAHKVVARA	888	
Qy	353 V-----SSELNNTTYST 364		
Db	889 TLRRSNVSRQRSSSLGGSTGST 910		
RESULT 5			
JC7683	taste receptor TIR3 - mouse C;Species: Mus musculus (house mouse)		
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004			
R;Kitagawa, M.; Kubakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A. Biochem. Biophys. Res. Commun. 283, 236-242, 2001 A;Title: Molecular genetic identification of a candidate receptor gene for sweet taste. A;Reference number: JC7683; MUID:21222875; PMID:11322794			
A;Contents: tongue A;Accession: JC7683 A;Molecule type: mRNA			
Qy	1 LPHSVCTTDVCPGTRGFVOREPICCFDSIPCAADGHVSRK-----GERECEQGEDYWS 555		
Db	504 VPTSQCSDPCAPNEMRN-MQPGDVCCWCIPC-----EPYEYLVDDEPTCMDCGPQWP 555		

Qy 56 NAQKSECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVHRRHTPLVNASDWQLG 115
 Db 556 TADLSGCYNLNPEDYIRWEDAWAIGPVTIAICLGFMCITCIVITVKHNNTPVKASGREIC 615

Qy 116 FLIQVSLIIMLSSMLFIDKPKNWSCMAGQVTLLALGSFLCLSLCLGKTSSLFLAYRISKS 175
 Db 616 YILLFGVSLSYCMIEFFIAKPSPVICALRRLGLGTSAICYSALLTKTNCIARIIDGVKN 675

Qy 176 KTQLTS-MHPLYRKIVLISVLAEGICAYLILEPPMV--YKNMESQNTKILLGNCNEIS 232
 Db 676 GAQRPKFISPPSSQVFLCLGLLQVIMVSVWLLTEPGTRRYTLPEKRET-VILKCNVKD 734

Qy 233 IEEFLYSMEFGIDAFLALLCFLTTFVARQLPDNYEYCKCITFGMLVFPFIWMSFPVYLSTK 292
 Db 735 SSMILSL-TYDWTLVIICLTVYAFKTRKCPENFNEAKFIGFTMYTCITIWLAFPLPIFYVTS 793

Qy 293 GKFKMAVEIFAILASSHG--LLGCIFAPKCLILLRPERNTSBEVCGRVSTTDNCIQLTS 350
 Db 794 SDYRVQTTTMCISVLSGFVVFLGCLFAPKVHIVLFQPQKN---VVTTHRLHNRFVSVSGTA 850

Db 351 AFVSELNNNTTVSTVLDDRVLI 372
 Qy 851 TTYSQSSASTYVPTVCNGREVL 872

RESULT 8
 JH0561 metabotropic Glutamate receptor 2 precursor - rat
 Db 794 SDYRVQTTTMCISVLSGFVVFLGCLFAPKVHIVLFQPQKN---VVTTHRLHNRFVSVSGTA 850

Qy 293 GKFKMAVEIFAILASSHG--LLGCIFAPKCLILLRPERNTSEIVCGRVSTTDNCIQLTS 350
 Db 735 SSMILSL-TYDWTLVIICLTVYAFKTRKCEFNPEAKFIGFTMYTCITIWLAFPLPIFYVTS 793

Qy 351 AFVSELNNNTTVSTVLDDRVLI 372
 Db 851 TTYSQSSASTYVPTVCNGREVL 872

RESULT 9
 JH0561 metabotropic Glutamate receptor 2 precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 R;Tanabe, Y.;Masu, M.;Ishii, T.;Shigemoto, R.;Nakanishi, S.
 A;Title: A family of metabotropic glutamate receptors.
 A;Reference number: JH0561; MUID:92110002; PMID:1309649
 A;Accession: JH0561
 A;Molecule type: mRNA
 A;Residues: 1-872 <TRAN>
 A;Cross-references: UNIPROT:P31421
 A;Experimental source: brain
 C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m
 C;Superfamily: metabotropic glutamate receptor 4
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
 F:568-590/Domain: transmembrane #status predicted <TRI>
 F:605-625/Domain: transmembrane #status predicted <TRI>
 F:637-655/Domain: transmembrane #status predicted <TRI>
 F:680-700/Domain: transmembrane #status predicted <TRV>
 F:726-747/Domain: transmembrane #status predicted <TRV>
 F:761-782/Domain: transmembrane #status predicted <TRV>
 F:795-819/Domain: transmembrane #status predicted <VII>
 F:203,286,338,402,547/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
 F:832/Binding site: phosphate (Thr) (covalent) #status predicted
 Query Match 20.6%; Score 409.5; DB 2; Length 872;
 Best Local Similarity 28.8%; Pred. No. 2.2e-25;
 Matches 109; Conservative 69; Mismatches 187; Indels 13; Gaps 8;

Qy 1 LPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQKS 60
 Db 495 LPASRCSEPCQLNEVKS-VQPGEVCWLCIPCQP--YBYRLDEFTCAADCGLGYWPNASLT 551

A;Experimental source: brain
 C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m
 C;Superfamily: metabotropic glutamate receptor 4
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
 F:577-599/Domain: transmembrane #status predicted <TRI>
 F:614-634/Domain: transmembrane #status predicted <TRI>
 F:646-664/Domain: transmembrane #status predicted <TRI>
 F:689-709/Domain: transmembrane #status predicted <TRV>
 F:735-756/Domain: transmembrane #status predicted <TRV>
 F:770-791/Domain: transmembrane #status predicted <TRV>
 F:804-828/Domain: transmembrane #status predicted <VII>
 F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted
 Query Match 20.9%; Score 415.5; DB 2; Length 879;
 Best Local Similarity 29.1%; Pred. No. 7.2e-26;
 Matches 111; Conservative 69; Mismatches 179; Indels 23; Gaps 9;

Qy 1 LPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWS 55
 Db 504 VPTSQCSDP CAPNEMKN-MQPGDyVCCWICIPC----EPYEYLVDDEFTCMDCGPQWP 555

Qy 56 NAQKSECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVHRRHTPLVNASDWQLG 115
 Db 556 TADLSGCYNLNPEDYIRWEDAWAIGPVTIAICLGFMCITCIVITVKHNNTPVKASGREIC 615

Qy 116 FLIQVSLIIMLSSMLFIDKPKNWSCMAGQVTLLALGSFLCLSLCLGKTSSLFLAYRISKS 175
 Db 616 YILLFGVSLSYCMIEFFIAKPSPVICALRRLGLGTSAICYSALLTKTNCIARIIDGVKN 675

Qy 176 KTQLTS-MHPLYRKIVLISVLAEGICAYLILEPPMV--YKNMESQNTKILLGNCNEIS 232

RESULT 9
 JC2132 metabotropic glutamate receptor 5 A - human
 C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
 C;Accession: JC2132 R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
 Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
 A;Title: Molecular cloning and the functional expression of two isoforms of human metabo
 A;Reference number: MUID:91156047; PMID:94197696; PMID:7908515
 A;Accession: JC2132
 A;Molecule type: mRNA
 A;Residues: 1-1180 <MIN>
 C;Comment: This protein is coupled to guanine nucleotide binding proteins.
 C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
 P;580-604/Domain: transmembrane #status predicted <TM1>
 P;617-637/Domain: transmembrane #status predicted <TM2>
 P;644-664/Domain: transmembrane #status predicted <TM3>
 P;694-714/Domain: transmembrane #status predicted <TM4>
 P;738-759/Domain: transmembrane #status predicted <TM5>
 P;773-794/Domain: transmembrane #status predicted <TM6>
 P;803-827/Domain: transmembrane #status predicted <TM7>
 Query Match 20.0%; Score 397.5; DB 2; Length 1199;
 Best Local Similarity 28.9%; Pred. No. 2.9e-24;
 Matches 99; Conservative 69; Mismatches 157; Indels 19; Gaps 7;
 QY 4 SVCTDVCPPGTGRGFQREPICCFDSDIPCADGHVSRKPGERECEQCGEDYWSNAQKSECV 63
 Db 522 SVCSEPCLKGQIKVIRKGEVSCCWICACKENEFVQ--DEFTCRACDLGWWPNAELTGCE 579
 QY 64 LKEVEYLAYDEALGFTLVLISVFGAFVFLAVTAVVYIHRHRTPLVNADWQLGFLIQVSLI 123
 Db 580 PIPVRYLEWSDIESIAIAFSCCLGLILVTLFPTLFLIVLYRDTPVVKSSSRELCYIILAGIF 639
 QY 124 IMLLSSMLPIDKPHNWSCMAGQVTLLALGSCLLSCUJGKTSSLFLAYRISKSKTQLTSMH 183
 Db 640 LGYVCVPFTLIAKPTTTSCTYQLRLLVGSSAMCYSALVTKTR--IARILAGSKKKICTRK 697
 QY 184 PLY----RKIVLIVLISVLAEGICTAYLILEPPMVKNMESQNTKILLGCNEISIEFLYS 238
 Db 698 PRFMSAWAQVIIASILISVQLTLVTLIIMEPPMPILSYPSIK-EVYLICNTSNLG-VVA 755
 QY 239 MFGIDAPFLALLCFLTFVARQLPDNYYEKGKCTIPGMLVFPIIWMSSFPVYVLSLKTKGKPKMA 298
 Db 756 PVGYNGLLIMSCTYYAKPTKTRNVPAFNFEAKYIAFTMYTCIIWIWLFVPIYFGS--NYKII 813
 QY 299 VEIFAILASSHGLLGCIPAPKCLLILLRPERN----TSEIV 335
 Db 814 TTCAFAVSLSVTTVALGCMFTPKYVIIIAKPERNVRSAFTTSDVV 856
 QY RESULT 11
 Db 627 LGYLCTFCLIAKPKQIYCYLQRIGIGLSAMSY SALVTKTR--IARILAGSKKKICTRK 684
 QY 184 PLY----RKIVLIVLISVLAEGICTAYLILEPPMVKNMESQNTKILLGCNEISIEFLYS 238
 Db 685 PRFMSACAQLVIAFILICIQLGIVIALFTIMEPPDIDMHDPSIR-EVYLICNTNLG-VVT 742
 QY 239 MFGIDAPFLALLCFLTFVARQLPDNYYEKGKCTIPGMLVFPIIWMSSFPVYVLSLKTKGKPKMA 298
 Db 743 PLGYNGLLISCTFYAFTKTRNVPAFNFEAKYIAFTMYTCIIWIWLFVPIYFGS--NYKII 800
 QY 299 VEIFAILASSHGLLGCIPAPKCLLILLRPERN----TSEIV 335
 Db 801 TMCFPSVSLSATVALGCMFVPKVIIILAKPERNVRSAFTTSTVV 843
 RESULT 10
 A41939 G protein-coupled glutamate receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A41939; S15362
 R;Houamed, K.M.; Kuijper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, Science 252, 1318-1321, 1991
 A;Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor
 A;Reference number: A41939; MUID:92022526; PMID:1656524
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-1199 <HOU>

A;Cross-references: UNIPROT:P23385; GB:M61099; NID:9397806; PID:AAA19497_1; PID:9204461
 A;Experimental source: cerebellum
 A;Note: sequence extracted from NCBI backbone (NCBIP:60785)
 R;Masu, M.; Tanabe, Y.; Tsuuchiida, K.; Shigemoto, R.; Nakaniishi, S.
 Nature 349, 760-765, 1991
 A;Title: Sequence and expression of a metabotropic glutamate receptor.
 A;Reference number: S15362; MUID:91156047; PMID:1847995
 A;Accession: S15362
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1199 <MAS>
 A;Cross-references: EMBL:X57569; NID:g56646; PID:CAA40799_1; PID:956647
 C;Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 20.0%; Score 397.5; DB 2; Length 1199;
 Best Local Similarity 28.6%; Pred. No. 2.9e-24;
 Matches 98; Conservative 69; Mismatches 157; Indels 19; Gaps 7;
 QY 4 SVCTDVCPPGTGRGFQREPICCFDSDIPCADGHVSRKPGERECEQCGEDYWSNAQKSECV 63
 Db 522 SVCSEPCLKGQIKVIRKGEVSCCWICACKENEFVQ--DEFTCRACDLGWWPNAELTGCE 579
 QY 64 LKEVEYLAYDEALGFTLVLISVFGAFVFLAVTAVVYIHRHRTPLVNADWQLGFLIQVSLI 123
 Db 580 PIPVRYLEWSDIESIAIAFSCCLGLILVTLFPTLFLIVLYRDTPVVKSSSRELCYIILAGIF 639
 QY 124 IMLLSSMLPIDKPHNWSCMAGQVTLLALGSCLLSCUJGKTSSLFLAYRISKSKTQLTSMH 183
 Db 640 LGYVCVPFTLIAKPTTTSCTYQLRLLVGSSAMCYSALVTKTR--IARILAGSKKKICTRK 697
 QY 184 PLY----RKIVLIVLISVLAEGICTAYLILEPPMVKNMESQNTKILLGCNEISIEFLYS 238
 Db 698 PRFMSAWAQVIIASILISVQLTLVTLIIMEPPMPILSYPSIK-EVYLICNTNLG-VVA 755
 QY 239 MFGIDAPFLALLCFLTFVARQLPDNYYEKGKCTIPGMLVFPIIWMSSFPVYVLSLKTKGKPKMA 298
 Db 756 PVGYNGLLIMSCTYYAKPTKTRNVPAFNFEAKYIAFTMYTCIIWIWLFVPIYFGS--NYKII 813
 QY 299 VEIFAILASSHGLLGCIPAPKCLLILLRPERN----TSEIV 335
 Db 814 TTCAFAVSLSVTTVALGCMFTPKYVIIIAKPERNVRSAFTTSDVV 856
 A;Accession: JC2131
 A;Molecule type: mRNA
 A;Residues: 1-11212 <MIN>
 C;Comment: This protein is coupled to guanine nucleotide binding proteins.
 C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
 C;Accession: JC2131 R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
 Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
 A;Title: Molecular cloning and the functional expression of two isoforms of human metabo
 A;Reference number: MUID:91156047; PMID:94197696; PMID:7908515
 A;Accession: JC2131
 A;Molecule type: mRNA
 A;Residues: 1-11212 <MIN>
 C;Comment: This protein is coupled to guanine nucleotide binding proteins.
 C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
 P;580-604/Domain: transmembrane #status predicted <TM1>
 P;617-637/Domain: transmembrane #status predicted <TM2>
 P;644-664/Domain: transmembrane #status predicted <TM3>
 P;694-714/Domain: transmembrane #status predicted <TM4>
 P;738-759/Domain: transmembrane #status predicted <TM5>
 P;773-794/Domain: transmembrane #status predicted <TM6>
 P;803-827/Domain: transmembrane #status predicted <TM7>
 Query Match 20.0%; Score 397.5; DB 2; Length 1212;
 Best Local Similarity 28.9%; Pred. No. 2.9e-24;
 Matches 99; Conservative 67; Mismatches 158; Indels 19; Gaps 7;
 QY 4 SVCTDVCPPGTGRGFQREPICCFDSDIPCADGHVSRKPGERECEQCGEDYWSNAQKSECV 63
 Db 509 SVCSEPCLKGQIKVIRKGEVSCCWICACKENEFVQ--DEFTCRACDLGWWPNAELTGCE 579
 QY 64 LKEVEYLAYDEALGFTLVLISVFGAFVFLAVTAVVYIHRHRTPLVNADWQLGFLIQVSLI 123
 Db 567 LIPVQYLRWGDPEPIAAVVFACLGILATLFTVVFIIYRDTPVVKSSSRELCYIILAGIC 626
 QY 124 IMLLSSMLPIDKPHNWSCMAGQVTLLALGSCLLSCUJGKTSSLFLAYRISKSKTQLTSMH 183
 Db 627 LGYLCTFCLIAKPKQIYCYLQRIGIGLSAMSY SALVTKTR--IARILAGSKKKICTRK 684
 QY 184 PLY----RKIVLIVLISVLAEGICTAYLILEPPMVKNMESQNTKILLGCNEISIEFLYS 238
 Db 685 PRFMSACAQLVIAFILICIQLGIVIALFTIMEPPDIDMHDPSIR-EVYLICNTNLG-VVT 742
 QY 239 MFGIDAPFLALLCFLTFVARQLPDNYYEKGKCTIPGMLVFPIIWMSSFPVYVLSLKTKGKPKMA 298
 Db 743 PLGYNGLLISCTFYAFTKTRNVPAFNFEAKYIAFTMYTCIIWIWLFVPIYFGS--NYKII 800
 QY 299 VEIFAILASSHGLLGCIPAPKCLLILLRPERN----TSEIV 335
 Db 801 TMCFPSVSLSATVALGCMFVPKVIIILAKPERNVRSAFTTSTVV 843
 RESULT 10
 A41939 G protein-coupled glutamate receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A41939; S15362
 R;Houamed, K.M.; Kuijper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, Science 252, 1318-1321, 1991
 A;Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor
 A;Reference number: A41939; MUID:92022526; PMID:1656524
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-1199 <HOU>

QY 64 LKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHTPLVNASDWQLGFLIQVSLI 123
 Db 567 LIPVQYLRWGDPEPIAAVVFACLGILLATLFTVTVFIIYRDTPVVKSSSRELCYIILAGIC 626

QY 124 IMLLSSMFLFDIKPHNWSCMAGQVTLAIGFSLCLSCLGKTSKTLAYRISKSKTQLTSMH 183
 Db 627 LGYLCTFCLIAKPQIYCYLQRIGIGLSPAMSYSALVTKTNR--TARILAGSKKKICTKK 684

QY 184 PLY----RKIIVLISVLAEGICLAYLILEPPPMVYKNCMESQNTKILGCNEISIEFLYS 238
 Db 685 PRFMSACAQLVIAFILICIQLGIIVALFIMEPPDIDMHDYPSTIR-EVYLICNTTNLG-VVT 742

QY 239 MFGIDARFLALLCFLTTFVARQLPDNYEGKCITFGMLVFFIIWMSFVPVYLSTKGKPKMA 298
 Db 743 PLGYNGLLISCTFYAFKTRNPANFNEAKYIAFTMYTCIIWIWAFVPIYFGS--NYKII 800

QY 299 VEIFAILASSHGLLGCIFAPKCLILLRPERN-----TSEIV 335
 Db 801 TMCFSVSLSATVALGCMFVPKVYIILAKPERNVSRAFTTSTVV 843

RESULT 12
 A42916 metabotropic glutamate receptor mGluR5 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A42916
 R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
 J. Biol. Chem. 267, 13361-13368, 1992
 A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5
 A;Reference number: A42916; MUID:92317054; PMID:1320017
 A;Accession: A42916
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1171 <ABE>
 A;Cross-references: UNIPROT:P31424; GB:D10891; NID:g220813; PIDN:BAA01711.1; PID:d100218
 A;Experimental source: brain
 A;Note: Sequence extracted from NCBI backbone (NCBIN:107749, NCBI:107750)
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.0%; Score 396.5; DB 2; Length 1171;
 Best Local Similarity 28.6%; Pred. No. 3.4e-24;
 Matches 98; Conservative 68; Mismatches 158; Indels 19; Gaps 7;

QY 4 SVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKGGERECEQGEDYWSNAQKSECV 63
 Db 508 SVCSEPCGEKGQIKVIRKGEVSCCWTCPKENEYVF--DEYTCKACQLGSWPTDDLTCGD 565

QY 64 LKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHTPLVNASDWQLGFLIQVSLI 123
 Db 566 LIPVQYLRWGDPEPIAAVVFACLGILLATLFTVTVFIIYRDTPVVKSSSRELCYIILAGIC 625

QY 124 IMLLSSMFLFDIKPHNWSCMAGQVTLAIGFSLCLSCLGKTSKTLAYRISKSKTQLTSMH 183
 Db 626 LGYLCTFCLIAKPQIYCYLQRIGIGLSPAMSYSALVTKTNR--TARILAGSKKKICTKK 683

QY 184 PLY----RKIIVLISVLAEGICLAYLILEPPPMVYKNCMESQNTKILGCNEISIEFLYS 238
 Db 684 PRFMSACAQLVIAFILICIQLGIIVALFIMEPPDIDMHDYPSTIR-EVYLICNTTNLG-VVT 741

QY 239 MFGIDARFLALLCFLTTFVARQLPDNYEGKCITFGMLVFFIIWMSFVPVYLSTKGKPKMA 298
 Db 742 PLGYNGLLISCTFYAFKTRNPANFNEAKYIAFTMYTCIIWIWAFVPIYFGS--NYKII 799

QY 299 VEIFAILASSHGLLGCIFAPKCLILLRPERN-----TSEIV 335
 Db 800 TMCFSVSLSATVALGCMFVPKVYIILAKPERNVSRAFTTSDVVRMVMVGDGTVACRSNSL 882

RESULT 13
 S71376 glutamate receptor homolog - cherry salmon

C;Species: Oncorhynchus masou (cherry salmon)
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
 C;Accession: S71376
 R;Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
 FEBS Lett. 392, 71-76, 1996
 A;Title: Cloning and characterization of a bifunctional metabotropic receptor activated
 A;Reference number: S71376; MUID:96354880; PMID:8769318
 A;Accession: S71376
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1218 <KUB>
 A;Cross-references: UNIPROT:Q90ZF3
 C;Keywords: glycoprotein; phosphoprotein
 F;603-625/Domain: transmembrane #status predicted <TM1>
 F;640-660/Domain: transmembrane #status predicted <TM2>
 F;672-690/Domain: transmembrane #status predicted <TM3>
 F;717-737/Domain: transmembrane #status predicted <TM4>
 F;761-782/Domain: transmembrane #status predicted <TM5>
 F;796-817/Domain: transmembrane #status predicted <TM6>
 F;826-850/Domain: transmembrane #status predicted <TM7>
 F;104,233,403,525,757/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;636,699,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F;892/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match 19.3%; Score 383; DB 2; Length 1218;
 Best Local Similarity 27.3%; Pred. No. 4.4e-23;
 Matches 98; Conservative 74; Mismatches 163; Indels 24; Gaps 8;

QY 4 SVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKGGERECEQGEDYWSNAQKSECV 63
 Db 532 SVCSEPCSKGEIKVIRKGEVSCCWTCACKDNETIVQ--DEFCTCTACDLGWWPDELEGCE 589

QY 64 LKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHTPLVNASDWQLGFLIQVSLI 123
 Db 590 PTLLRYLEWGNPESIVQYVFACLGILVTSFVTFFIFVLYRDTPVVKSSRELCYTILLAGIF 649

QY 124 IMLISSMFLFDKPHNWSCMAGQVTLAIGFSLCLSCLGKTSKTLAYRISKSKTQLTSMH 183
 Db 650 LGYICPFTLIAOPTVASCYLORLVLGLSATWCYSAVLTCTNR--TARILAGSKKKICTRK 707

QY 184 PLY----RKIIVLISVLAEGICLAYLILEPPPMVYKNCMESQNTKILGCNEISIEFLYS 238
 Db 708 PRFMSAWAQLVIAQLVAGLLWSVOLTLEVTLILEPPMPVKSYPSPSR-EVFLICNTSTVG-MVA 765

QY 239 MFGIDARFLALLCFLTTFVARQLPDNYEGKCITFGMLVFFIIWMSFVPVYLSTKGKPKMA 298
 Db 766 PLGYNGLLIMSLMSCTYYAFKTRNVPAFNNEAKYIAFTMYTCIIWLAFVPIYFGS--NYKII 823

QY 299 VEIFAILASSHGLLGCIFAPKCLILLRPERN-----TSEIV-----TSEIV 346
 Db 824 TTFSVSLSVTVALGCMFSPKIVIILAKPERNVSRAFTTSDVVRMVMVGDGTVACRSNSL 882

RESULT 14
 T27628 hypothetical protein ZC506.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T27628
 R;Harris, B.
 Submitted to the EMBL Data Library, December 1994
 A;Reference number: Z20395
 A;Accession: T27628
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-999 <WIL>
 A;Cross-references: UNIPROT:Q09630; EMBL:Z47073; PIDN:CAA87374.1; GSPDB:GN00028; CESP:ZC
 C;Genetics:
 A;Gene: CESP:ZC506.4
 A;Map position: X
 A;Introns: 32/2; 65/3; 77/3; 113/2; 140/3; 177/2; 240/2; 277/1; 315/2; 439/2; 471/3; 591/

C;Superfamily: metabotropic glutamate receptor 4

Query Match 17.8%; Score 353; DB 2; Length 999;
Best Local Similarity 26.3%; Pred. No. 9.8e-21;
Matches 98; Conservative 75; Mismatches 179; Indels 20; Gaps 11;

Qy 2 PHSVCTDVCPPGTRGFVQRREPICCFDSIPCADGHVSRKGERECEQCGEDYWSNAQKSE 61
Db 607 PVSVCSPCKPKQLIKDEQ-CCWACSKCDE--YEYLINETHCVGCEQWWPTKDKKG 663

Qy 62 CV---LKEVEYLAYDEALGFTLVLSVGAFFVVLAVTAVVYIHRHTPLVNASDWQLGFLIQV 120
Db 664 CFDLSQLKYMWRMSMYSLVPTILAVFGLIATLFLVIVVVVYINETPVWKASGRELSYIL 723

Qy 119 QVSLLIMLSSMLFDKPHNWSCMAGQVTIALGFSLCLSCLLGKTSSLFLAYRISKSKTQ 178
Db 724 LISIMIMCYCMTFVLLSKPSAIVCAIKRTGIGFAFSCLYSAMFVKTNRIFRIFS-TRSAQR 782

Qy 179 LTMHMHFLYRKIIIVLISVLAEGIICTA--YLIPEPMVYKNMBSQNTKILGCICFAPKCLILLRPERNTSE 333
Db 783 PRFISFISQ--VVMTAMLGVQLIGSLIWLWVPP-GWRHHYPTRDQVWLTCNVPDHHFPL 839

Qy 237 YSMFGIDAFALLCFLTTFVARQLPNDNYEGKCCRITFGMLVFFIWNMSFVPPVYLSTTKGKFK 296
Db 840 YSL-AYDGFLIVLCTTYAVKTRKVPEFNNETKPIGFSMYTTCVWVLSWIFFFFGTGSDFQ 898

Qy 297 MAVE--IFAILASMSGHLGCIIFAPKCLILLRPERNT---SEIVCGRVS-TTDNCIQLT 349
Db 899 IQTSSLCISMSANVALAACIFSPKLWILFEKXONVRKQEGESMLNKSSRSLGNCSSRL 958

Qy 350 SAFVSSELNNNT 361
Db 959 CANSIDEPNQYT 970

RESULT 15
A49874

metabotropic glutamate receptor 7 - rat
N;Alternate names: metabotropic glutamate receptor mGluR7
C;Species: Rattus norvegicus (Norway, rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A49874; 157954
R;Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakaniishi, J. Biol. Chem. 269, 1231-1236, 1994
A;Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 couple
A;Reference number: A49874; PMID:94117433; PMID:8288585
A;Accession: A49874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-915 <RES>
A;Cross-references: UNIPROT:P35400; GB:D16817; NID:9458728; PID:BAA04092.1; PID:g458729
R;Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
Mol. Pharmacol. 45, 367-372, 1994
A;Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A;Reference number: 157954; PMID:94195260; PMID:8145723
A;Accession: 157954
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-915 <RE2>
C;Genetics:
A;Gene: MGLUR7
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: neurotransmitter receptor

Query Match 16.3%; Score 324; DB 2; Length 915;
Best Local Similarity 26.1%; Pred. No. 2e-18;
Matches 93; Conservative 71; Mismatches 153; Indels 40; Gaps 12;

Qy 1 LPHSVCTDVCPPGTRGFVOREPICFDSTPCADGHVSRKPGRECEQCGEDYWSNAQKS 60
Db 518 IPSSVCTLPCPKPGQ-RKKTFQGTPCCWTCEPC-DGY-QIQFDEMTQHCPCPYDQRPNENRT 574

THIS PAGE LEFT BLANK